RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _10/536,875,_
Source: _PCT/10_
Date Processed by STIC: _6/9/05_

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 06/09/2005
PATENT APPLICATION: US/10/536,875   TIME: 09:39:42

Input Set : A:\038136-5001-US Sequence Listing.txt
Output Set: N:\CRF4\06092005\J536875.raw

```
   3 <110> APPLICANT: BRIGGS, Kristen
   4        GLANCY, Todd
   5        HEIN, Mitch B.
   6        HIATT, Andrew C.
   7        KARNOUP, Anton S.
   8        ANDERSON, W.H. Kerr
   9        PAREDDY, Dayakar
  10        PETOLINO, Joseph
  11        RUBIN-WILSON, Elizabeth
  12        TAYLOR, Doug
  13        Roberts, Jean L.
  14        The Dow Chemical Company
  15        Dow Agrosciences, LLC
  16        Epicyte Pharmaceutical, Inc.
  18 <120> TITLE OF INVENTION: Plant production of immunoglobulins with reduced
fucosylation
  20 <130> FILE REFERENCE: 038136-5001-US
C--> 22 <140> CURRENT APPLICATION NUMBER: US/10/536,875
C--> 22 <141> CURRENT FILING DATE: 2005-05-27
  22 <150> PRIOR APPLICATION NUMBER: US 60/429,385
  23 <151> PRIOR FILING DATE: 2002-11-27
  25 <150> PRIOR APPLICATION NUMBER: PCT/US03/037905
  26 <151> PRIOR FILING DATE: 2003-11-28
  28 <160> NUMBER OF SEQ ID NOS: 85
  30 <170> SOFTWARE: PatentIn version 3.1
  32 <210> SEQ ID NO: 1
  33 <211> LENGTH: 1494
  34 <212> TYPE: DNA
  35 <213> ORGANISM: Herpes simplex virus
  37 <220> FEATURE:
  38 <221> NAME/KEY: CDS
  39 <222> LOCATION: (1)..(1494)
  41 <220> FEATURE:
  42 <221> NAME/KEY: misc_feature
  43 <223> OTHER INFORMATION: HSV Heavy Chain sequence
  46 <400> SEQUENCE: 1
  47 atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt        48
  48 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
  49 1               5                   10                  15
  51 gtc cat tgc cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag        96
  52 Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
  53              20                  25                  30
  55 cct ggc tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc       144
  56 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
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57          35                    40                    45
59 agc tcc tat gct atc aac tgg gtg agg caa gct cct gga caa ggg ctt    192
60 Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
61     50                    55                    60
63 gag tgg atg gga ggg ctc atg cct atc ttt ggg aca aca aac tac gcg    240
64 Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
65 65                    70                    75                    80
67 cag aag ttc cag gac agg ctc acg att acc gcg gac gta tcc acg agt    288
68 Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
69                    85                    90                    95
71 aca gcc tac atg caa ctg agc ggc ctg aca tat gaa gac acg gcc atg    336
72 Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
73                    100                   105                   110
75 tat tac tgt gcg aga gtt gcc tac atg ctt gaa cct acc gtc act gca    384
76 Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
77          115                   120                   125
79 ggt ggt ttg gac gtc tgg ggc caa ggg acc ttg gtc acc gtc tcc tcc    432
80 Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
81     130                   135                   140
83 gca tcc ccg acc agc ccg aag gtc ttc ccg ctg agc ctc tgt agc acc    480
84 Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
85·145                   150                   155                   160
87 cag cca gat ggg aac gtg gtc atc gcc tgc ctg gtc cag ggc ttc ttc    528
88 Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
89                    165                   170                   175
91 cct cag gag cca ctc agt gtg acc tgg agc gaa agc gga cag ggc gtg    576
92 Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
93          180                   185                   190
95 acc gcc agg aac ttc cca ccc agc cag gat gcc tcc gga gac ctg tac    624
96 Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
97          195                   200                   205
99 acc acg tcc agc cag ctg acc ctt ccg gcc aca cag tgc cta gcg ggc    672
100 Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
101    210                   215                   220
103 aag tcc gtg aca tgc cac gtg aag cac tac acg aat ccc agc cag gat   720
104 Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
105 225                   230                   235                   240
107 gtg act gtg ccc tgc cca gtt ccc tca act cca cct acc cca tct ccc   768
108 Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
109                   245                   250                   255
111 tcg act cca cct acc cca tct ccc tca tgc tgc cac ccc agg ctg tca   816
112 Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
113                   260                   265                   270
115 ctg cac agg cct gcc ctc gag gac ctg ctc tta ggt tcg gaa gcg aac   864
116 Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
117          275                   280                    ·        285
119 ctc acg tgc aca ctc acc ggc ctg aga gat gcg tca ggt gtc acc ttc   912
120 Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
121    290                   295                   300
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123 acc tgg acg ccc tca agt ggt aag agc gct gtt caa ggc cca cct gag    960
124 Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
125 305             310             315             320
127 cgt gac ctc tgt ggc tgc tac agc gtg tcc agt gtc ctt ccg ggc tgt    1008
128 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
129             325             330             335
131 gcc gag cct tgg aat cat ggg aag acc ttc act tgc act gct gcc tac    1056
132 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
133             340             345             350
135 ccc gag agc aag acc ccg cta acc gcc acc ctc tcg aaa tcc ggc aac    1104
136 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
137             355             360             365
139 aca ttc cgg ccc gag gtc cac ctg ctg ccg ccg ccg tcg gag gag ctg    1152
140 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
141     370             375             380
143 gcc ctg aac gag ctg gtg acg ctg acg tgc ctg gcg cgc ggc ttc agc    1200
144 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
145 385             390             395             400
147 ccc aag gac gtg ctg gtt cgc tgg ctg cag ggc tca cag gag ctg cct    1248
148 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
149             405             410             415
151 agg gag aag tac ctg act tgg gca tcc cgg cag gag ccc agc caa ggc    1296
152 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
153             420             425             430
155 acc acc acc ttc gct gtg acc tcg ata ctg cgc gtg gca gcc gag gac    1344
156 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
157             435             440             445
159 tgg aag aag ggt gac acc ttc tcc tgc atg gtg ggc cac gag gcc ctt    1392
160 Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
161     450             455             460
163 ccg ctg gcc ttc aca cag aag acc atc gac cgc ttg gcg ggt aaa ccc    1440
164 Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
165 465             470             475             480
167 acc cat gtc aat gtg tct gtt gtc atg gcg gag gtg gac ggc acc tgc    1488
168 Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
169             485             490             495
171 tac tga                                                           1494
172 Tyr
176 <210> SEQ ID NO: 2
177 <211> LENGTH: 497
178 <212> TYPE: PRT
179 <213> ORGANISM: Herpes simplex virus
181 <400> SEQUENCE: 2
183 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
184 1               5               10              15
187 Val His Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
188             20              25              30
191 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe
192             35              40              45
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195 Ser Ser Tyr Ala Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
196     50              55              60
199 Glu Trp Met Gly Gly Leu Met Pro Ile Phe Gly Thr Thr Asn Tyr Ala
200 65              70              75              80
203 Gln Lys Phe Gln Asp Arg Leu Thr Ile Thr Ala Asp Val Ser Thr Ser
204             85              90              95
207 Thr Ala Tyr Met Gln Leu Ser Gly Leu Thr Tyr Glu Asp Thr Ala Met
208             100             105             110
211 Tyr Tyr Cys Ala Arg Val Ala Tyr Met Leu Glu Pro Thr Val Thr Ala
212         115             120             125
215 Gly Gly Leu Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
216     130             135             140
219 Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr
220 145             150             155             160
223 Gln Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe
224             165             170             175
227 Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val
228             180             185             190
231 Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr
232         195             200             205
235 Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly
236     210             215             220
239 Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp
240 225             230             235             240
243 Val Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro
244             245             250             255
247 Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser
248             260             265             270
251 Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn
252         275             280             285
255 Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe
256     290             295             300
259 Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Glu
260 305             310             315             320
263 Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys
264             325             330             335
267 Ala Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr
268             340             345             350
271 Pro Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn
272         355             360             365
275 Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu
276     370             375             380
279 Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser
280 385             390             395             400
283 Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro
284             405             410             415
287 Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly
288         420             425             430
291 Thr Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp
```

```
292          435                440                445
295 Trp Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu
296     450                455                460
299 Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro
300 465            470                475                480
303 Thr His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys
304              485                490                495
307 Tyr
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 57
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: Heavy chain signal peptide
319 <220> FEATURE:
320 <221> NAME/KEY: CDS
321 <222> LOCATION: (1)..(57)
323 <400> SEQUENCE: 3
324 atg gga tgg agc tgg atc ttt ctc ttc ctc ctg tca gga gct gca ggt      48
325 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
326 1             5                10                15
328 gtc cat tgc                                                           57
329 Val His Cys
333 <210> SEQ ID NO: 4
334 <211> LENGTH: 19
335 <212> TYPE: PRT
336 <213> ORGANISM: Artificial sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Heavy chain signal peptide
341 <400> SEQUENCE: 4
343 Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Ala Ala Gly
344 1             5                10                15
347 Val His Cys
351 <210> SEQ ID NO: 5
352 <211> LENGTH: 1368
353 <212> TYPE: DNA
354 <213> ORGANISM: Artificial sequence
356 <220> FEATURE:
357 <223> OTHER INFORMATION: Mature heavy chain sequence
359 <220> FEATURE:
360 <221> NAME/KEY: CDS
361 <222> LOCATION: (1)..(1368)
363 <400> SEQUENCE: 5
364 cag gtt cag ctc gtg cag tca ggt gct gag gtg aag aag cct ggc tcc      48
365 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
366 1             5                10                15
368 tcg gtg aag gtc tcc tgc aag gct tct gga ggt tcc ttc agc tcc tat      96
369 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Ser Phe Ser Ser Tyr
370              20                25                30
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/09/2005
PATENT APPLICATION: **US/10/536,875**   TIME: 09:39:43

Input Set : **A:\038136-5001-US Sequence Listing.txt**
Output Set: **N:\CRF4\06092005\J536875.raw**

<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:85; N Pos. 9895,9989,10099

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/536,875**

DATE: 06/09/2005
TIME: 09:39:43

Input Set : **A:\038136-5001-US Sequence Listing.txt**
Output Set: **N:\CRF4\06092005\J536875.raw**

```
L:22 M:270 C: Current Application Number differs, Replaced Current Application No
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:9840
M:341 Repeated in SeqNo=85
```